

0550
01/02

OIPE

RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/802,472A

TIME: 15:07:04

Input Set : A:\EINAT4.1C.txt

Output Set: N:\CRF3\01032002\I802472A.raw

P.S

3 <110> APPLICANT: EINAT, Paz
 4 SKALITER, Rami
 5 FEINSTEIN, Elena
 7 <120> TITLE OF INVENTION: SEQUENCES CHARACTERISTIC OF HYPOXIA-REGULATED GENE
 TRANSCRIPTION

9 <130> FILE REFERENCE: EINAT=4.1C
 11 <140> CURRENT APPLICATION NUMBER: US/09/802,472A
 11 <141> CURRENT FILING DATE: 2001-03-09
 11 <150> PRIOR APPLICATION NUMBER: US 09/383,096
 12 <151> PRIOR FILING DATE: 1999-08-27
 14 <150> PRIOR APPLICATION NUMBER: US 09/138,109
 15 <151> PRIOR FILING DATE: 1998-08-21
 17 <150> PRIOR APPLICATION NUMBER: US 60/098,158
 18 <151> PRIOR FILING DATE: 1998-08-27
 20 <150> PRIOR APPLICATION NUMBER: US 60/132,684
 21 <151> PRIOR FILING DATE: 1999-05-05
 23 <160> NUMBER OF SEQ ID NOS: 21
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1655
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (265)..(1575)
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: (5)..(5)
 39 <223> OTHER INFORMATION: "n" is unknown
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 44 <222> LOCATION: (22)..(22)
 45 <223> OTHER INFORMATION: "n" is unknown
 48 <220> FEATURE:
 49 <221> NAME/KEY: misc_feature
 50 <222> LOCATION: (41)..(41)
 51 <223> OTHER INFORMATION: "n" is unknown
 54 <220> FEATURE:
 55 <221> NAME/KEY: misc_feature
 56 <222> LOCATION: (47)..(47)
 57 <223> OTHER INFORMATION: "n" is unknown
 60 <400> SEQUENCE: 1

ENTERED

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 63 ggcgcaggag gggtcgcggg gagggagtgg tgagcgcagg cggcaggggt ctgggaaaga 120
 65 cgaagtcgct atttgctgtc tgagcgcgct cgcagctcct ggaagtgttg ccgcctctcg 180
 67 gtttcgctct cgctcgctgc gctcctagaa ggggcggccg cctccaggac tgaccagggc 240
 69 caagtggcgc tcggcgggca ctac atg gcg gag ggt gaa ggg tac ttc gcc 291
 70 Met Ala Glu Gly Glu Gly Tyr Phe Ala

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71                                1                                5
73 atg tct gag gac gag ctg gcc tgc agc ccc tac atc ccc cta ggc ggc      339
74 Met Ser Glu Asp Glu Leu Ala Cys Ser Pro Tyr Ile Pro Leu Gly Gly
75 10                                15                                20                                25
77 gac ttc ggc ggc ggc gac ttc ggc ggc ggc gac ttc ggc ggt ggc ggc      387
78 Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Gly
79                                30                                35                                40
81 agc ttc ggt ggg cat tgc ttg gac tat tgc gaa agc cct acg gcg cac      435
82 Ser Phe Gly Gly His Cys Leu Asp Tyr Cys Glu Ser Pro Thr Ala His
83                                45                                50                                55
85 tgc aat gtg ctg aac tgg gag caa gtg cag cgg ctg gac ggc atc ctg      483
86 Cys Asn Val Leu Asn Trp Glu Gln Val Gln Arg Leu Asp Gly Ile Leu
87                                60                                65                                70
89 agc gag acc att ccg att cac ggg cgc ggc aac ttc ccc acg ctc gag      531
90 Ser Glu Thr Ile Pro Ile His Gly Arg Gly Asn Phe Pro Thr Leu Glu
91                                75                                80                                85
93 ctg cag ccg agc ctg atc gtg aag gtg gtg cgg cgg cgc ctg gcc gag      579
94 Leu Gln Pro Ser Leu Ile Val Lys Val Val Arg Arg Arg Leu Ala Glu
95 90                                95                                100                                105
97 aag cgc att ggc gtc cgc gac gtg cgc ctc aac ggc tcg gca gcc agc      627
98 Lys Arg Ile Gly Val Arg Asp Val Arg Leu Asn Gly Ser Ala Ala Ser
99                                110                                115                                120
101 cat gtc ctg cac cag gac agc ggc ctg ggc tac aag gac ctg gac ctc      675
102 His Val Leu His Gln Asp Ser Gly Leu Gly Tyr Lys Asp Leu Asp Leu
103                                125                                130                                135
105 atc ttc tgc gcc gac ctg cgc ggg gaa ggg gag ttt cag act gtg aag      723
106 Ile Phe Cys Ala Asp Leu Arg Gly Glu Gly Glu Phe Gln Thr Val Lys
107                                140                                145                                150
109 gac gtc gtg ctg gac tgc ctg ttg gac ttc tta ccc gag ggg gtg aac      771
110 Asp Val Val Leu Asp Cys Leu Leu Asp Phe Leu Pro Glu Gly Val Asn
111                                155                                160                                165
113 aaa gag aag atc aca cca ctc acg ctc aag gaa gct tat gtg cag aaa      819
114 Lys Glu Lys Ile Thr Pro Leu Thr Leu Lys Glu Ala Tyr Val Gln Lys
115 170                                175                                180                                185
117 atg gtt aaa gtg tgc aat gac tct gac cga tgg agt ctt ata tcc ctg      867
118 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
119                                190                                195                                200
121 tca aac aac agt ggc aaa aat gtg gaa ctg aaa ttt gtg gat tcc ctc      915
122 Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
123                                205                                210                                215
125 cgg agg cag ttt gaa ttc agt gta gat tct ttt caa atc aaa tta gac      963
126 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
127                                220                                225                                230
129 tct ctt ctg ctc ttt tat gaa tgt tca gag aac cca atg act gag aca      1011
130 Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
131                                235                                240                                245
133 ttt cac ccc aca ata atc ggg gag agc gtc tat ggc gat ttc cag gaa      1059
134 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
135 250                                255                                260                                265

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```

137 gcc ttt gat cac ctt tgt aac aag atc att gcc acc agg aac cca gag      1107
138 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
139                               270                               275                               280
141 gaa atc cga ggg gga ggc ctg ctt aag tac tgc aac ctc ttg gtg agg      1155
142 Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
143                               285                               290                               295
145 ggc ttt agg ccc gcc tct gat gaa atc aag acc ctt caa agg tat atg      1203
146 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met
147                               300                               305                               310
149 tgt tcc agg ttt ttc atc gac ttc tca gac att gga gag cag cag aga      1251
150 Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
151                               315                               320                               325
153 aaa ctg gag tcc tat ttg cag aac ctc ttt gtg gga ttg gaa gcc cgc      1299
154 Lys Leu Glu Ser Tyr Leu Gln Asn Leu Phe Val Gly Leu Glu Ala Arg
155 330                               335                               340                               345
157 aag tat gag tat ctc atg acc ctt cat gga gtg gta aat gag agc tca      1347
158 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Ser
159                               350                               355                               360
161 gtg tgc ctg atg gga cat gaa aga aga cag act tta aac ctt atc acc      1395
162 Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
163                               365                               370                               375
165 atg ctg gct atc cgg gtg tta gct gac caa aat gtc att cct aat gtg      1443
166 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
167                               380                               385                               390
169 gct aat gtc act tgc tat tac cag cca gcc ccc tat gta gca gat gcc      1491
170 Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
171                               395                               400                               405
173 aac ttt agc aat tac tac att gca cag gtt cag cca gta ttc acg tgc      1539
174 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
175 410                               415                               420                               425
177 cag caa cag acc tac tcc act tgg cta ccc tgc aat taagaatcat      1585
178 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn
179                               430                               435
181 ttaaaaaatgt cctgtgggga agccatttca gacaagacag gagagaaaaa aaaaaaaaaa      1645
183 aaaaaaaaaa      1655
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 437
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 2
193 Met Ala Glu Gly Glu Gly Tyr Phe Ala Met Ser Glu Asp Glu Leu Ala
194 1                               5                               10                               15
197 Cys Ser Pro Tyr Ile Pro Leu Gly Gly Asp Phe Gly Gly Gly Asp Phe
198                               20                               25                               30
201 Gly Gly Gly Asp Phe Gly Gly Gly Ser Phe Gly Gly His Cys Leu
202                               35                               40                               45
205 Asp Tyr Cys Glu Ser Pro Thr Ala His Cys Asn Val Leu Asn Trp Glu
206                               50                               55                               60
209 Gln Val Gln Arg Leu Asp Gly Ile Leu Ser Glu Thr Ile Pro Ile His

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210 65          70          75          80
213 Gly Arg Gly Asn Phe Pro Thr Leu Glu Leu Gln Pro Ser Leu Ile Val
214          85          90          95
217 Lys Val Val Arg Arg Arg Leu Ala Glu Lys Arg Ile Gly Val Arg Asp
218          100          105          110
221 Val Arg Leu Asn Gly Ser Ala Ala Ser His Val Leu His Gln Asp Ser
222          115          120          125
225 Gly Leu Gly Tyr Lys Asp Leu Asp Leu Ile Phe Cys Ala Asp Leu Arg
226          130          135          140
229 Gly Glu Gly Glu Phe Gln Thr Val Lys Asp Val Val Leu Asp Cys Leu
230 145          150          155          160
233 Leu Asp Phe Leu Pro Glu Gly Val Asn Lys Glu Lys Ile Thr Pro Leu
234          165          170          175
237 Thr Leu Lys Glu Ala Tyr Val Gln Lys Met Val Lys Val Cys Asn Asp
238          180          185          190
241 Ser Asp Arg Trp Ser Leu Ile Ser Leu Ser Asn Asn Ser Gly Lys Asn
242          195          200          205
245 Val Glu Leu Lys Phe Val Asp Ser Leu Arg Arg Gln Phe Glu Phe Ser
246          210          215          220
249 Val Asp Ser Phe Gln Ile Lys Leu Asp Ser Leu Leu Leu Phe Tyr Glu
250 225          230          235          240
253 Cys Ser Glu Asn Pro Met Thr Glu Thr Phe His Pro Thr Ile Ile Gly
254          245          250          255
257 Glu Ser Val Tyr Gly Asp Phe Gln Glu Ala Phe Asp His Leu Cys Asn
258          260          265          270
261 Lys Ile Ile Ala Thr Arg Asn Pro Glu Glu Ile Arg Gly Gly Gly Leu
262          275          280          285
265 Leu Lys Tyr Cys Asn Leu Leu Val Arg Gly Phe Arg Pro Ala Ser Asp
266          290          295          300
269 Glu Ile Lys Thr Leu Gln Arg Tyr Met Cys Ser Arg Phe Phe Ile Asp
270 305          310          315          320
273 Phe Ser Asp Ile Gly Glu Gln Gln Arg Lys Leu Glu Ser Tyr Leu Gln
274          325          330          335
277 Asn Leu Phe Val Gly Leu Glu Ala Arg Lys Tyr Glu Tyr Leu Met Thr
278          340          345          350
281 Leu His Gly Val Val Asn Glu Ser Ser Val Cys Leu Met Gly His Glu
282          355          360          365
285 Arg Arg Gln Thr Leu Asn Leu Ile Thr Met Leu Ala Ile Arg Val Leu
286          370          375          380
289 Ala Asp Gln Asn Val Ile Pro Asn Val Ala Asn Val Thr Cys Tyr Tyr
290 385          390          395          400
293 Gln Pro Ala Pro Tyr Val Ala Asp Ala Asn Phe Ser Asn Tyr Tyr Ile
294          405          410          415
297 Ala Gln Val Gln Pro Val Phe Thr Cys Gln Gln Gln Thr Tyr Ser Thr
298          420          425          430
301 Trp Leu Pro Cys Asn
302          435
305 <210> SEQ ID NO: 3
306 <211> LENGTH: 3454

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307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
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314 <220> FEATURE:
315 <221> NAME/KEY: misc_feature
316 <222> LOCATION: (606)..(606)
317 <223> OTHER INFORMATION: "n" is unknown
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321 <221> NAME/KEY: misc_feature
322 <222> LOCATION: (2561)..(2561)
323 <223> OTHER INFORMATION: "n" is unknown
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (2594)..(2504)
329 <223> OTHER INFORMATION: "n" is unknown
332 <220> FEATURE:
333 <221> NAME/KEY: misc_feature
334 <222> LOCATION: (2613)..(2613)
335 <223> OTHER INFORMATION: "n" is unknown
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341 tccgagggcg tgaaaacccc tgcgctgcgg cccttcccag gccccgagg cgttcgccg      120
343 ttcccgaagc ccgactgggg gaagagtcca gcaccaaagc ggccgttctc ggattccgga      180
345 gcgttctgga gccccgagag acgccccggg gttctagaag ctccccggcg gcgccagtc      240
347 cgggttcat tcgggcgtcc ctccgaaacc cactcgggtg cacgggtcgt cggcgagccg      300
349 cgaccgggtc ctggcgcgca cc atg atc gtg gcg gac tcc gag tgc cgc gca      352
350                               Met Ile Val Ala Asp Ser Glu Cys Arg Ala
351                               1           5           10
353 gag ctc aag gac tac ctg cgg ttc gcc ccg ggc ggc gtc ggc gac tcg      400
354 Glu Leu Lys Asp Tyr Leu Arg Phe Ala Pro Gly Gly Val Gly Asp Ser
355                               15           20           25
357 ggc ccc gga gag gag cag agg gag agc cgg gct cgg cga ggc cct cga      448
358 Gly Pro Gly Glu Glu Gln Arg Glu Ser Arg Ala Arg Arg Gly Pro Arg
359                               30           35           40
361 ggg ccc agc gcc ttc atc ccc gtg gag gag gtc ctt cgg gag ggg gct      496
362 Gly Pro Ser Ala Phe Ile Pro Val Glu Glu Val Leu Arg Glu Gly Ala
363                               45           50           55
365 gag agc ctc gag cag cac ctg ggg ctg gag gca ctg atg tcc tct ggg      544
366 Glu Ser Leu Glu Gln His Leu Gly Leu Glu Ala Leu Met Ser Ser Gly
367                               60           65           70
369 cga gta gac aac ctg gca gtg gtg atg ggc ctg cac cct gac tac ttt      592
370 Arg Val Asp Asn Leu Ala Val Val Met Gly Leu His Pro Asp Tyr Phe
371 75                               80           85           90
w- 373 acc agc ttc tgg cnc ctg cac tac ctg ctg ctg cac acg gat ggt ccc      640
w--> 374 Thr Ser Phe Trp Xaa Leu His Tyr Leu Leu His Thr Asp Gly Pro
375                               95           100          105
377 ttg gcc agc tcc tgg cgc cac tac att gcc atc atg gct gcc gcc cgc      688

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\EINAT4.1C.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:2618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:2631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20